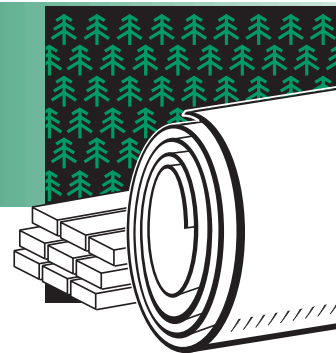


# FOREST PRODUCTS

## Project Fact Sheet



### PINE GENE DISCOVERY PROJECT

#### BENEFITS

- Preparation of a catalogue of pine genes useful as reagents and diagnostic tools for industrial research
- Development of knowledge for studying fundamental problems in pine physiology and the species' resistance to disease and environmental stress
- Advancement of biological information concerning the similarity of genes among major taxonomic groups of plants and animals

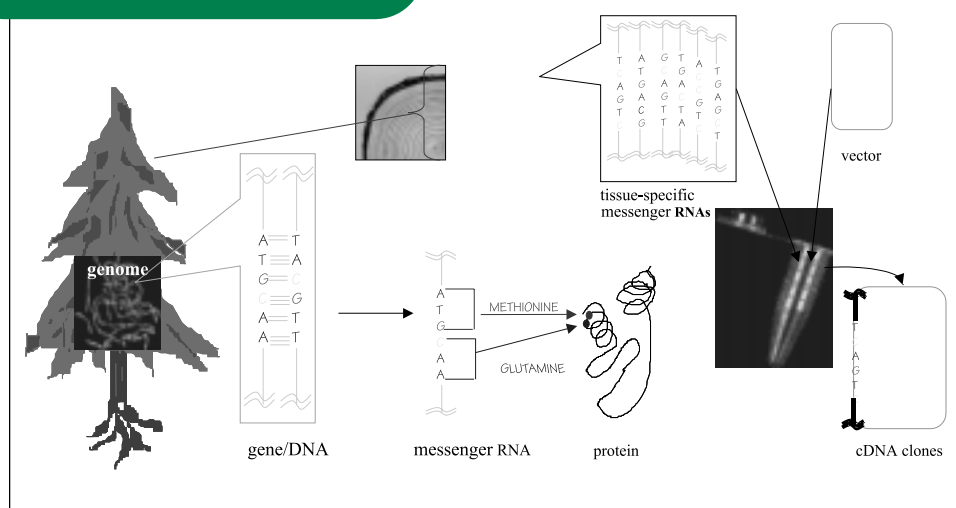
#### APPLICATIONS

Locating large numbers of pine genes and identifying the traits they control will provide industry with the potential to improve the planting stock for loblolly pine. The future genetic engineering of trees that are disease-resistant, and/or that have new fiber characteristics, will help the U.S. forest products industry improve its long-term economic competitiveness.

### IDENTIFYING PINE GENES WILL PROVIDE A RESOURCE FOR IMPROVING LOBLOLLY PINE STOCKS

Identification of large numbers of partial gene sequences in woody plants will open up new scientific and commercial opportunities for the forestry industry, similar to the way gene identification has revolutionized the biomedical industry. Research into the gene sequences of major agricultural plants is already underway, but there is a lack of fundamental information on the structure, identity, and function of genes in woody plants. Access to a catalogue of loblolly pine genes will be an important asset to forestry researchers, allowing studies to proceed on the genetic engineering of improved tree lines, the control of specific properties of trees, and on other opportunities to improve plant stocks. It will also be valuable to foresters pursuing commercial application of the new knowledge.

#### PINE GENE DISCOVERY PROJECT



**All cells contain all the genes (in the form of DNA) required by the entire organism. Genes are expressed to produce proteins with specific cellular functions. Gene expression results in production of messenger RNA, which can be captured *in vitro* as cDNA. These short cDNA sequences are sufficient to suggest gene function by comparison to database sequences.**



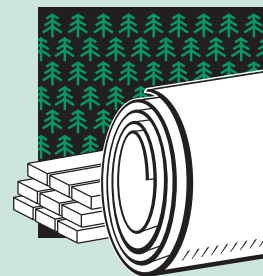
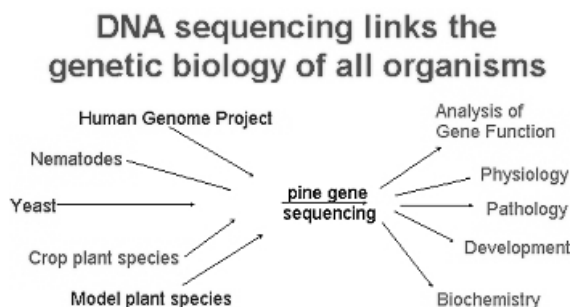
## Project Description

**Goal:** To isolate, partially sequence, and attempt to determine the functions of as many of the genes expressed in loblolly pine genes as possible.

Research plans call for cloning and partially sequencing about 10,000 cDNAs, representing about 8,000 unique loblolly pine genes. A variety of samples will be taken at different developmental stages from different tissues and organs of a single pine genotype, and a new experimental approach will be used to maximize the number of genes identified while reducing the cost of the identification process. This will be a three-year effort involving four principal investigators who represent three separate research institutions.

## Progress & Milestones

- The first year will be spent making libraries, establishing the procedures for reducing the previously sequenced and abundantly expressed genes in cDNA libraries, and beginning the collection of sequencing data.
- The majority of the sequencing data will be collected in the second and third year of the project.
- Computers will be used to match identified genes with possible functions, and all the information generated will be put into a database on the Internet.
- The cDNA clones used for sequencing determination will be provided to researchers in industries and public institutions that support the Gene Discovery Project, to help further their research activities.
- Weekly updates on analyzed data will be available to interested researchers during the second and third year of the project.



## PROJECT PARTNERS

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North Carolina State University  
University of Minnesota  
Georgia-Pacific Corporation  
Rayonier Corporation  
Union Camp Corporation  
Westvaco Corporation

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October 1998